In the claims:

Claims 1-26 **(canceled)**

27. **(currently amended)** A method for identifying drug candidates comprising:

(a) transforming a first set of host cells with ~~the~~ a first set of plasmids, ~~of claim 1~~ each plasmid comprising a first mutant rRNA gene and a first selectable marker gene;

wherein said mutant rRNA gene comprises at least one mutation and a first mutant Anti-Shine-Dalgarno sequence; and said first selectable marker gene comprises a first mutant Shine-Dalgarno sequence; and

wherein said first mutant Anti-Shine-Dalgarno sequence and said first mutant Shine-Dalgarno sequence are a mutually compatible pair;

thereby forming a first set of transformed host cells;

(b) isolating from the first set of transformed host cells those host cells [[via]] which express the selectable marker gene product;

(c) ~~identifying and~~ sequencing the first mutant rRNA gene from each host cell isolated in step (b) to identify ~~the~~ regions of interest, wherein the regions of interest comprise sequences of one or more nucleic acids which are conserved in each first mutant rRNA gene sequenced;

~~(d) selecting regions of interest from step (c);~~

~~(e)~~ (d) generating a second plurality of mutant rRNA genes wherein ~~mutating~~ the regions of interest from step (c) are mutated; and each rRNA gene further comprises a second mutant Anti-Shine-Dalgarno sequence;

~~(f)~~ (e) inserting the second plurality of mutant rRNA genes comprising the mutated regions of interest from step ~~(e)~~ (d) into a second plurality of plasmids; wherein said plasmids further comprise ~~comprising an rRNA gene having a mutant Anti-Shine-Dalgarno sequence and~~ a second genetically engineered gene which encodes a second selectable marker having a second mutant Shine-Dalgarno sequence, wherein the second mutant Anti-Shine-Dalgarno and the second mutant Shine-Dalgarno sequence are a mutually compatible pair;

~~(g)~~ (f) transforming [[a]] a second set of host cells with the plasmids from step ~~(f)~~ (e), thereby forming a second set of transformed host cells;

~~(h)~~ (g) isolating from the second set of transformed host cells from step ~~(g)~~ (f) [[via]] those host cells which express the selectable marker gene product;

~~(i)~~ (h) ~~identifying~~ sequencing the rRNA gene from each host cell isolated in step ~~(h)~~ (g) to identify the mutated regions of interest ~~functional mutant ribosomes~~;

~~(j)~~ (i) screening drug candidates against the mutated regions of interest ~~functional mutant ribosomes~~ from step ~~(i)~~ (h) and the wildtype rRNA;

~~(k)~~ (j) identifying the drug candidates from step ~~(j)~~ (i) that ~~bound~~ bind to the mutated regions of interest ~~functional mutant ribosomes~~ from step ~~(i)~~ (h) and the wildtype rRNA;

~~(l)~~ (k) screening the drug candidates from step ~~(k)~~ (j) against a human rRNA; and

~~(m)~~ (l) identifying the drug candidates from step ~~(l)~~ (k) that do not bind to the human rRNA, thereby identifying drug candidates.

28. **(currently amended)** A method for identifying drug candidates comprising:

(a) transforming a first set of host cells with ~~the~~ a first set of plasmids, ~~of claim 1~~ each plasmid comprising a first mutant *E. coli* 16S rRNA gene and a first selectable marker gene;

wherein said mutant *E. coli* 16S rRNA gene comprises at least one mutation and a first mutant Anti-Shine-Dalgarno sequence; and said first selectable marker gene comprises a first mutant Shine-Dalgarno sequence; and

wherein said first mutant Anti-Shine-Dalgarno sequence and said first mutant Shine-Dalgarno sequence are a mutually compatible pair;

thereby forming a first set of transformed host cells;

(b) isolating from the first set of transformed host cells those host cells [[via]] which express the selectable marker gene product;

(c) ~~identifying and~~ sequencing the first mutant rRNA gene from each host cell isolated in step (b) to identify ~~the~~ regions of interest, wherein the regions of

interest comprise sequences of one or more nucleic acids which are conserved in each first mutant rRNA gene sequenced;

~~(d) selecting regions of interest from step (c);~~

~~(e)~~ (d) generating a second plurality of mutant rRNA genes wherein ~~mutating~~ the regions of interest from step (c) are mutated; and each rRNA gene further comprises a second mutant Anti-Shine-Dalgarno sequence;

~~(f)~~ (e) inserting the second plurality of mutant *E. coli* 16S rRNA genes comprising the mutated regions of interest from step ~~(e)~~ (d) into a second plurality of plasmids; wherein said plasmids further comprise ~~comprising an *E. coli* 16S rRNA gene having a mutant Anti-Shine-Dalgarno sequence and~~ a genetically engineered gene which encodes ~~GFP~~ green fluorescent protein having a second mutant Shine-Dalgarno sequence, wherein the second mutant Anti-Shine-Dalgarno and the second mutant Shine-Dalgarno sequence are a mutually compatible pair;

~~(g)~~ (f) transforming [[a]] a second set of host cells with the plasmids from step ~~(f)~~ (e), thereby forming a second set of transformed host cells;

~~(h)~~ (g) isolating from the second set of transformed host cells from step ~~(g)~~ (f) [[via]] those host cells which express ~~the selectable marker~~ a genetically engineered gene which encodes green fluorescent protien;

~~(i)~~ (h) ~~identifying~~ sequencing the rRNA genes from each host cell isolated in step ~~(h)~~ (g) to identify the mutated regions of interest ~~functional mutant ribosomes~~;

~~(j)~~ (i) screening drug candidates against the the mutated regions of interest ~~functional mutant ribosomes~~ from step ~~(i)~~ (h) and the wildtype 16S rRNA;

~~(k)~~ (j) identifying the drug candidates from step ~~(j)~~ (i) that ~~bound~~ bind to the mutated regions of interest ~~functional mutant ribosomes~~ from step ~~(i)~~ (h) and the wildtype 16S rRNA;

~~(l)~~ (k) screening the drug candidates from step ~~(k)~~ (j) against a human 16S rRNA; and

~~(m)~~ (l) identifying the drug candidates from step ~~(l)~~ (k) that do not bind to the human 16S rRNA, thereby identifying drug candidates.

Claims 29-36 **(canceled)**

37. (**new**) The method of claim 27, wherein said first mutant rRNA gene is selected from the rRNA genes of *Escherichia coli, Mycobacterium tuberculosis, Pseudomonas aeruginosa, Salmonella typhi, Yersenia pestis, Staphylococcus aureus, Streptococcus pyogenes, Enterococcus faecalis, Chlamydia trachomatis, Saccharomyces cerevesiae, Candida albicans,* and trypanosomes.

38. (**new**) The method of claim 27, wherein said first mutant rRNA gene is a 16S rRNA gene.

39. (**new**) The method of claim 27, wherein said first mutant Shine-Dalgarno sequence is selected from the group consisting of the sequences set forth in SEQ. ID. NOS: 24-159.

40. (**new**) The method of claim 27, wherein said first mutant Anti-Shine-Dalgarno sequence is selected from the group consisting of the sequences set forth in SEQ. ID. NOS: 24-159.

41. (**new**) The method of claim 27, wherein said second mutant Shine-Dalgarno sequence is selected from the group consisting of the sequences set forth in SEQ. ID. NOS: 24-159.

42. (**new**) The method of claim 27, wherein said second mutant Anti-Shine-Dalgarno sequence is selected from the group consisting of the sequences set forth in SEQ. ID. NOS: 24-159.

43. (**new**) The method of claim 27, wherein said first selectable marker is selected from the group consisting of chloramphenicol acetyltransferase (CAT), green fluorescent protein (GFP), or both.

44. (**new**) The method of claim 27, wherein said second selectable marker is selected from the group consisting of chloramphenicol acetyltransferase (CAT), green fluorescent protein (GFP), or both.

45. (**new**) The method of claim 28, wherein said first mutant Shine-Dalgarno sequence is selected from the group consisting of the sequences set forth in SEQ. ID. NOS: 24-159.

46. (**new**) The method of claim 28, wherein said first mutant Anti-Shine-Dalgarno sequence is selected from the group consisting of the sequences set forth in SEQ. ID. NOS: 24-159.

47. (**new**) The method of claim 28, wherein said second mutant Shine-Dalgarno sequence is selected from the group consisting of the sequences set forth in SEQ. ID. NOS: 24-159.

48. (**new**) The method of claim 28, wherein said second mutant Anti-Shine-Dalgarno sequence is selected from the group consisting of the sequences set forth in SEQ. ID. NOS: 24-159.

49. (**new**) The method of claim 28, wherein said first selectable marker is selected from the group consisting of chloramphenicol acetyltransferase (CAT), green fluorescent protein (GFP), or both.